



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/009,445B
Source: IFW16
Date Processed by STIC: 10-12-04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 06/05/04):
U.S. Patent and Trademark Office, 220 20th Street S., Customer Window, Mail Stop Sequence, Crystal Plaza Two, Lobby, Room 1B03, Arlington, VA 22202

Revised 05/17/04

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleic Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was received in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 <input type="checkbox"/> Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 <input type="checkbox"/> Misaligned Amino Numbering	The numbering under each 5 th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 <input type="checkbox"/> Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 <input type="checkbox"/> Variable Length	Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>.<223> section that some may be missing	
6 <input type="checkbox"/> PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>.<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>.<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>.<223> sections for Artificial or Unknown sequences.	
7 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence (2) INFORMATION FOR SEQ ID NO:X (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS (Do not insert any subheadings under this heading!) (ii) SEQUENCE DESCRIPTION SEQ ID NO X (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped	
	Please also adjust the "(ii) NUMBER OF SEQUENCES" response to include the skipped sequence.	
8 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence <210> sequence id number <400> sequence id number 000	
9 <input type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing Per 1.823 of Sequence Rules, use of <220>.<223> is MANDATORY if n's or Xaa's are present in <220> to <223> section. Please explain location of n or Xaa, and which residue n or Xaa represents	
10 <input checked="" type="checkbox"/> Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are Unknown, Artificial Sequence, or scientific name (Genus/species) <220>.<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 <input type="checkbox"/> Use of <220>	Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See, "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 <input type="checkbox"/> PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 <input type="checkbox"/> Misuse of n/Xaa	"n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid	



IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,445B

DATE: 10/12/2004

TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
 Output Set: N:\CRF4\10122004\J009445B.raw

4 <110> APPLICANT: BARCLAY, A. Neil
 5 BROWN, Marion H.
 6 GORMAN, Daniel M.
 7 LANIER, Lewis L.
 8 WRIGHT, Gavin J.
 9 CHERWINSKI, Holly
 10 PHILLIPS, Joseph H.
 11 HOEK, Robert M.
 12 SEDGWICK, Jonathan D.
 14 <120> TITLE OF INVENTION: OX2 RECEPTOR HOMOLOGS (AS AMENDED)
 16 <130> FILE REFERENCE: 140942000900
 18 <140> CURRENT APPLICATION NUMBER: US 10/009,445B
 19 <141> CURRENT FILING DATE: 2001-11-13
 21 <150> PRIOR APPLICATION NUMBER: PCT US00/12998
 22 <151> PRIOR FILING DATE: 2000-05-11
 24 <150> PRIOR APPLICATION NUMBER: GB 9925989.7
 25 <151> PRIOR FILING DATE: 1999-11-03
 28 <150> PRIOR APPLICATION NUMBER: GB 9911123.9
 29 <151> PRIOR FILING DATE: 1999-05-13
 31 <160> NUMBER OF SEQ ID NOS: 70
 33 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 36 <210> SEQ ID NO: 1
 37 <211> LENGTH: 1574
 38 <212> TYPE: DNA
 39 <213> ORGANISM: Unknown
 41 <220> FEATURE:
 42 <223> OTHER INFORMATION: Description of Unknown Organism: rodent; surmised
 43 rattus rattus
 45 <220> FEATURE:
 46 <221> NAME/KEY: CDS
 47 <222> LOCATION: (91)..(1071)
 49 <220> FEATURE:
 50 <221> NAME/KEY: mat_peptide
 51 <222> LOCATION: (162)..(1071)
 53 <400> SEQUENCE: 1
 54 agcggaggga tcctggcat ggtcacccgt gctcccctac ctgtgaagag aaagaggcacc 60
 55 gagtgagccg ctgaaaacca gaaaaccgaa atg ctc tgc ttt tgg aga act tct 114
 57 Met Leu Cys Phe Trp Arg Thr Ser
 58 -20
 60 cac gta gca gta ctc ttg atc tgg ggg gtc ttc gcg gct gag tca agt 162
 61 His Val Ala Val Leu Ile Trp Gly Val Phe Ala Ala Glu Ser Ser
 62 -15 -10 -5 -1
 64 tgt cct gat aag aat caa aca atg cag aac aat tca tca act atg aca 210

(pg.6-7)
 Does Not Comply
 Corrected Diskette Needed

(pg.3,6)

RAW SEQUENCE LISTING

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TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
 Output Set: N:\CRF4\10122004\J009445B.raw

65	Cys	Pro	Asp	Lys	Asn	Gln	Thr	Met	Gln	Asn	Asn	Ser	Ser	Thr	Met	Thr	
66	1			5			10			15							
68	gaa	gtt	aac	act	aca	gtg	ttt	gta	cag	atg	ggt	aaa	aag	gct	ctg	ctc	258
69	Glu	Val	Asn	Thr	Thr	Val	Phe	Val	Gln	Met	Gly	Lys	Lys	Ala	Leu	Leu	
70				20				25			30						
72	tgc	tgc	cct	tct	att	tca	ctg	aca	aaa	gta	ata	tta	ata	aca	tgg	aca	306
73	Cys	Cys	Pro	Ser	Ile	Ser	Leu	Thr	Lys	Val	Ile	Leu	Ile	Thr	Trp	Thr	
74				35				40			45						
76	ata	acc	ctc	aga	gga	cag	cct	tcc	tgc	ata	ata	tcc	tac	aaa	gca	gac	354
77	Ile	Thr	Leu	Arg	Gly	Gln	Pro	Ser	Cys	Ile	Ile	Ser	Tyr	Lys	Ala	Asp	
78				50				55			60						
80	aca	agg	gag	acc	cat	gaa	agc	aac	tgc	tcg	gac	aga	agc	atc	acc	tgg	402
81	Thr	Arg	Glu	Thr	His	Glu	Ser	Asn	Cys	Ser	Asp	Arg	Ser	Ile	Thr	Trp	
82	65				70			75			80						
84	gcc	tcc	aca	cct	gac	ctc	gct	cct	gac	ctt	cag	atc	agt	gca	gtg	gcc	450
85	Ala	Ser	Thr	Pro	Asp	Leu	Ala	Pro	Asp	Leu	Gln	Ile	Ser	Ala	Val	Ala	
86				85				90			95						
88	ctc	cag	cat	gaa	ggg	cgt	tac	tca	tgt	gat	ata	gca	gta	cct	gac	ggg	498
89	Leu	Gln	His	Glu	Gly	Arg	Tyr	Ser	Cys	Asp	Ile	Ala	Val	Pro	Asp	Gly	
90				100				105			110						
92	aat	ttc	caa	aac	atc	tat	gac	ctc	caa	gtg	ctg	gtg	ccc	cct	gaa	gta	546
93	Asn	Phe	Gln	Asn	Ile	Tyr	Asp	Leu	Gln	Val	Leu	Val	Pro	Pro	Glu	Val	
94				115				120			125						
96	acc	cac	ttt	cca	ggg	gaa	aat	aga	act	gca	gtt	tgt	gag	gcg	att	gca	594
97	Thr	His	Phe	Pro	Gly	Glu	Asn	Arg	Thr	Ala	Val	Cys	Glu	Ala	Ile	Ala	
98				130				135			140						
100	ggc	aaa	cct	gct	gcg	cag	atc	tct	tgg	acg	cca	gat	ggg	gat	tgt	gtc	642
101	Gly	Lys	Pro	Ala	Ala	Gln	Ile	Ser	Trp	Thr	Pro	Asp	Gly	Asp	Cys	Val	
102	145				150				155			160					
104	gct	aag	aat	gaa	tca	cac	agc	aat	ggc	acc	gtg	act	gtc	cgg	agc	aca	690
105	Ala	Lys	Asn	Glu	Ser	His	Ser	Asn	Gly	Thr	Val	Thr	Val	Arg	Ser	Thr	
106					165				170			175					
108	tgc	cac	tgg	gag	cag	agc	cac	gtg	tct	gtc	gtg	ttc	tgt	gtt	gtc	tct	738
109	Cys	His	Trp	Glu	Gln	Ser	His	Val	Ser	Val	Val	Phe	Cys	Val	Val	Ser	
110				180				185			190						
112	cac	ttg	aca	act	ggt	aat	cag	tct	ctg	tct	ata	gaa	ctg	ggt	aga	ggg	786
113	His	Leu	Thr	Thr	Gly	Asn	Gln	Ser	Leu	Ser	Ile	Glu	Leu	Gly	Arg	Gly	
114				195				200			205						
116	ggt	gac	caa	tta	tta	gga	tca	tac	att	caa	tac	atc	atc	cca	tct	att	834
117	Gly	Asp	Gln	Leu	Leu	Gly	Ser	Tyr	Ile	Gln	Tyr	Ile	Ile	Pro	Ser	Ile	
118				210				215			220						
120	att	att	ttg	atc	atc	ata	gga	tgc	att	tgt	ctt	ttg	aaa	atc	agt	ggc	882
121	Ile	Ile	Leu	Ile	Ile	Ile	Gly	Cys	Ile	Cys	Leu	Leu	Lys	Ile	Ser	Gly	
122	225				230				235			240					
124	tgc	aga	aaa	tgt	aaa	ttg	cca	aaa	tcg	gga	gct	act	cca	gat	att	gag	930
125	Cys	Arg	Lys	Cys	Lys	Leu	Pro	Lys	Ser	Gly	Ala	Thr	Pro	Asp	Ile	Glu	
126				245				250			255						
128	gag	gat	gaa	atg	cag	ccg	tat	gct	agc	tac	aca	gag	aag	agc	aat	cca	978
129	Glu	Asp	Glu	Met	Gln	Pro	Tyr	Ala	Ser	Tyr	Thr	Glu	Lys	Ser	Asn	Pro	

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Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
Output Set: N:\CRF4\10122004\J009445B.raw

130 260 265 270
 132 ctc tat gat act gtg acc acg acg gag gca cac cca gcg tca caa ggc 1026
 133 Leu Tyr Asp Thr Val Thr Thr Glu Ala His Pro Ala Ser Gln Gly
 134 275 280 285
 136 aaa gtc aat ggc aca gac tgt ctt act ttg tca gcc atg gga atc 1071
 137 Lys Val Asn Gly Thr Asp Cys Leu Thr Leu Ser Ala Met Gly Ile
 138 290 295 300
 140 tagaaccaag gaaaagaagt caagagacat cataattact gctttcttt ctttaaactt 1131
 142 ctccaatgga gggaaattag ctctctgaa gttcttagaa agcacaatg ttctaatgga 1191
 144 ttgcctta agttctcta tcatttggaaatg ttgttgcattt ttatggtaaa atatcaaatt 1251
 146 tagaagaac tgatttaattt attacaaaga aagcacattt ttatggtaaa atatcaaatt 1311
 148 gtcaataca atgatgaaaaa ctgagttcc tcaagaaata actgcagaag gaacaatcat 1371
 150 tactaaagca tttcatgtga gttcttccaa aaaagaaaaat ccctgtgtat acgacatgtat 1431
 152 tatggatgt gtgtgcctt atatgttgc ttacaaatgt gtatatatgc acacatctga 1491
 154 ttatcaagac atctctgtca aaaactcaact ggcgttccag atttatgaaa gctaataaag 1551
 156 tgagtattgg agatgttttata 1574

159 <210> SEQ ID NO: 2

160 <211> LENGTH: 327

161 <212> TYPE: PRT

162 <213> ORGANISM: Unknown

W--> 164 <220> FEATURE:

W--> 164 <223> OTHER INFORMATION:

W--> 164 <400> 2

165 Met Leu Cys Phe Trp Arg Thr Ser His Val Ala Val Leu Leu Ile Trp
 166 -20 -15 -10
 168 Gly Val Phe Ala Ala Glu Ser Ser Cys Pro Asp Lys Asn Gln Thr Met
 169 -5 -1 1 5
 171 Gln Asn Asn Ser Ser Thr Met Thr Glu Val Asn Thr Thr Val Phe Val
 172 10 15 20
 174 Gln Met Gly Lys Lys Ala Leu Leu Cys Cys Pro Ser Ile Ser Leu Thr
 175 25 30 35 40
 177 Lys Val Ile Leu Ile Thr Trp Thr Ile Thr Leu Arg Gly Gln Pro Ser
 178 45 50 55
 180 Cys Ile Ile Ser Tyr Lys Ala Asp Thr Arg Glu Thr His Glu Ser Asn The type of errors shown exist throughout
 181 60 65 70 the Sequence Listing. Please check subsequent
 183 Cys Ser Asp Arg Ser Ile Thr Trp Ala Ser Thr Pro Asp Leu Ala Pro sequences for similar errors.
 184 75 80 85
 187 Asp Leu Gln Ile Ser Ala Val Ala Leu Gln His Glu Gly Arg Tyr Ser
 188 90 95 100
 190 Cys Asp Ile Ala Val Pro Asp Gly Asn Phe Gln Asn Ile Tyr Asp Leu
 191 105 110 115 120
 193 Gln Val Leu Val Pro Pro Glu Val Thr His Phe Pro Gly Glu Asn Arg
 194 125 130 135
 196 Thr Ala Val Cys Glu Ala Ile Ala Gly Lys Pro Ala Ala Gln Ile Ser
 197 140 145 150
 199 Trp Thr Pro Asp Gly Asp Cys Val Ala Lys Asn Glu Ser His Ser Asn
 200 155 160 165
 202 Gly Thr Val Thr Val Arg Ser Thr Cys His Trp Glu Gln Ser His Val
 203 170 175 180

Pls see error explanation on page 8. ✓

Pls insert, whenever <213> response
is artificial
Unknown or
Genus/Species.

↑
 The type of errors shown exist throughout
 the Sequence Listing. Please check subsequent
 sequences for similar errors.

RAW SEQUENCE LISTING
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Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
Output Set: N:\CRF4\10122004\J009445B.raw

205 Ser Val Val Phe Cys Val Val Ser His Leu Thr Thr Gly Asn Gln Ser
206 185 190 195 200
208 Leu Ser Ile Glu Leu Gly Arg Gly Gly Asp Gln Leu Leu Gly Ser Tyr
209 205 210 215
211 Ile Gln Tyr Ile Ile Pro Ser Ile Ile Ile Ile Ile Gly Cys
212 220 225 230
214 Ile Cys Leu Leu Lys Ile Ser Gly Cys Arg Lys Cys Lys Leu Pro Lys
215 235 240 245
217 Ser Gly Ala Thr Pro Asp Ile Glu Asp Glu Met Gln Pro Tyr Ala
218 250 255 260
220 Ser Tyr Thr Glu Lys Ser Asn Pro Leu Tyr Asp Thr Val Thr Thr Thr
221 265 270 275 280
223 Glu Ala His Pro Ala Ser Gln Gly Lys Val Asn Gly Thr Asp Cys Leu
224 285 290 295
226 Thr Leu Ser Ala Met Gly Ile
227 300
230 <210> SEQ ID NO: 3
231 <211> LENGTH: 1604
232 <212> TYPE: DNA
233 <213> ORGANISM: Unknown
235 <220> FEATURE:
236 <223> OTHER INFORMATION: Description of Unknown Organism: primate; surmised
237 homo sapiens
239 <220> FEATURE:
240 <221> NAME/KEY: CDS
241 <222> LOCATION: (217)..(1101)
243 <220> FEATURE:
244 <221> NAME/KEY: mat_peptide
245 <222> LOCATION: (295)..(1101)
247 <400> SEQUENCE: 3
248 cagagaaaag cttctgttcg tccaagttac taaccaggct aaaccacata gacgtgaagg 60
250 aaggggctag aaggaaggga gtgccccact gttgatgggg taagaggatc ctgtactgag 120
252 aagttgacca gagagggtct caccatgcgc acagttcctt ctgtaccagt gtggaggaaa 180
254 agtactgagt gaagggcaga aaaagagaaa acagaa atg ctc tgc cct tgg aga 234
255 Met Leu Cys Pro Trp Arg
256 -25
258 act gct aac cta ggg cta ctg ttg att ttg act atc ttc tta gtg gcc 282
259 Thr Ala Asn Leu Gly Leu Leu Ile Leu Thr Ile Phe Leu Val Ala
260 -20 -15 -10 -5
262 gaa gcg gag ggt gct gct caa cca aac aac tca tta atg ctg caa act 330
263 Glu Ala Glu Gly Ala Ala Gln Pro Asn Asn Ser Leu Met Leu Gln Thr
264 -1 1 5 10
266 agc aag gag aat cat gct tta gct tca agc agt tta tgt atg gat gaa 378
267 Ser Lys Glu Asn His Ala Leu Ala Ser Ser Leu Cys Met Asp Glu
268 15 20 25
270 aaa cag att aca cag aac tac tcg aaa gta ctc gca gaa gtt aac act 426
271 Lys Gln Ile Thr Gln Asn Tyr Ser Lys Val Leu Ala Glu Val Asn Thr
272 30 35 40
274 tca tgg cct gta aag gct aca aat gct gtg ctt tgt tgc cct cct 474

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/009,445B

DATE: 10/12/2004

TIME: 11:51:41

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
 Output Set: N:\CRF4\10122004\J009445B.raw

275 Ser Trp Pro Val Lys Met Ala Thr Asn Ala Val Leu Cys Cys Pro Pro
 276 45 50 55 60
 278 atc gca tta aga aat ttg atc ata ata aca tgg gaa ata atc ctg aga 522
 279 Ile Ala Leu Arg Asn Leu Ile Ile Ile Thr Trp Glu Ile Ile Leu Arg
 280 65 70 75
 282 ggc cag cct tcc tgc aca aaa gcc tac aag aaa gaa aca aat gag acc 570
 283 Gly Gln Pro Ser Cys Thr Lys Ala Tyr Lys Lys Glu Thr Asn Glu Thr
 284 80 85 90
 286 aag gaa acc aac tgt act gat gag aga ata acc tgg gtc tcc aga cct 618
 287 Lys Glu Thr Asn Cys Thr Asp Glu Arg Ile Thr Trp Val Ser Arg Pro
 288 95 100 105
 290 gat cag aat tcg gac ctt cag att cgt acc gtc gac atc act cat gac 666
 291 Asp Gln Asn Ser Asp Leu Gln Ile Arg Thr Val Ala Ile Thr His Asp
 292 110 115 120
 294 ggg tat tac aga tgc ata atg gta aca cct gat ggg aat ttc cat cgt 714
 295 Gly Tyr Tyr Arg Cys Ile Met Val Thr Pro Asp Gly Asn Phe His Arg
 296 125 130 135 140
 298 gga tat cac ctc caa gtc tta gtt aca cct gaa gtc acc ctg ttt caa 762
 299 Gly Tyr His Leu Gln Val Leu Val Thr Pro Glu Val Thr Leu Phe Gln
 300 145 150 155
 302 aac agg aat aga act gca gta tgc aag gca gtt gca ggg aag cca gct 810
 303 Asn Arg Asn Arg Thr Ala Val Cys Lys Ala Val Ala Gly Lys Pro Ala
 304 160 165 170
 306 gcg cat atc tcc tgg atc cca gag ggc gat tgt gtc act aag caa gaa 858
 307 Ala His Ile Ser Trp Ile Pro Glu Gly Asp Cys Ala Thr Lys Gln Glu
 308 175 180 185
 310 tac tgg agc aat ggc aca gtc act gtt aag agt aca tgc cac tgg gag 906
 311 Tyr Trp Ser Asn Gly Thr Val Thr Val Lys Ser Thr Cys His Trp Glu
 312 190 195 200
 314 gtc cac aat gtc tct acc gtc acc tgc cac gtc tcc cat ttg act ggc 954
 315 Val His Asn Val Ser Thr Val Thr Cys His Val Ser His Leu Thr Gly
 316 205 210 215 220
 318 aac aag agt ctg tac ata gag cta ctt cct gtt cca ggt gcc aaa aaa 1002
 319 Asn Lys Ser Leu Tyr Ile Glu Leu Leu Pro Val Pro Gly Ala Lys Lys
 320 225 230 235
 322 atc agc aaa att ata tat tcc ata tat cat cct tac tat tat tat tta 1050
 323 Ile Ser Lys Ile Ile Tyr Ser Ile Tyr His Pro Tyr Tyr Tyr Leu
 324 240 245 250
 326 gac cat cgt ggg att cat ttg gtt gaa agt caa tgg ctg cag aaa 1098
 327 Asp His Arg Gly Ile His Leu Val Val Glu Ser Gln Trp Leu Gln Lys
 328 255 260 265
 330 ata taaattgaat aaaacagaat ctactccagt tggaggag gatgaaatgc 1151
 331 Ile
 333 agccctatgc cagctacaca gagaagaaca atcctctcta tgatactaca aacaaggta 1211
 335 aggcatctga ggcattacaa agtgaagttt acacagacct ccatacttta taagttttt 1271
 337 gactcttagta ccaagaaaca acaacaaacg agatacattta taattactgt ctgattttct 1331
 339 tacagttcta gaatgaagac ttatattgaa attagttttt ccaaggttct tagaagacat 1391
 341 ttaatggat tctcattcat accctgtat aattggaaatt ttgattttt agctgctacc 1451
 343 agcttagttct ctgaagaact gatgttatta caaagaaaat acatgccccat gaccaaatat 1511

<210> 21
<211> 1044
<212> DNA
<213> reverse translation

<220>
<221> misc_feature
<222> (1)..(1044)
<223> n may be a, c, g, or t

<400> 21

INVALID
Response

Mandatory, <213>

Responses has to be
either artificial/
Unknown or Genus/
Species. Pls see
item # 10 on
error summary
Sheet.

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/12/2004
PATENT APPLICATION: US/10/009,445B TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
Output Set: N:\CRF4\10122004\J009445B.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 6,18,21,24,30,33,36,39,42,51,54,60,63,69,72,78,93,108,111
Seq#:13; N Pos. 114,120,126,132,135,138,144,153,162,165,168,177,180,186,189
Seq#:13; N Pos. 192,198,204,210,216,222,225,228,231,237,240,252,261,267,270
Seq#:13; N Pos. 276,285,294,300,303,309,315,318,321,324,330,333,336,342,351
Seq#:13; N Pos. 354,357,360,363,375,378,384,396,399,402,408,432,438,441,444
Seq#:13; N Pos. 447,450,456,459,468,471,480,483,486,489,498,504,507,513,516
Seq#:13; N Pos. 519,528,534,537,543,552,555,567,573,579,582,585,588,591,594
Seq#:13; N Pos. 597,600,618,624,627,630,633,642,645,648,654,657,660,663,672
Seq#:13; N Pos. 675,678,687,690,693,696,699,708,711,714,717,738,741,753,765
Seq#:13; N Pos. 777,780,789,792,798,810,813,819,822,825,828,831,858,864,867
Seq#:13; N Pos. 873,882,888,891,900,903,906,909,912,918,924,927,930,936,942
Seq#:13; N Pos. 948,951,960,963,966,969,972,978
Seq#:14; N Pos. 6,12,18,21,24,30,33,36,39,42,48,51,60,63,66,72,78,81,84,90
Seq#:14; N Pos. 99,102,108,114,117,132,135,138,141,144,147,150,174,186,192
Seq#:14; N Pos. 195,198,204,210,213,219,222,231,234,240,243,246,255,258,264
Seq#:14; N Pos. 267,270,276,288,303,306,309,315,318,324,330,345,354,363,372
Seq#:14; N Pos. 381,387,393,396,399,402,414,420,429,432,435,438,444,453,462
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Seq#:14; N Pos. 552,558,561,564,567,576,579,582,585,591,594,597,606,615,621
Seq#:14; N Pos. 630,633,651,657,660,663,666,669,675,678,693,702,705,708,711
Seq#:14; N Pos. 714,723,726,732,735,738,747,750,762,765,768,771,774,777,780
Seq#:14; N Pos. 792,807,819,834,843,846,855,858,861,867,876
Seq#:15; N Pos. 18,21,24,27,30,33,36,39,42,51,54,60,63,66,69,72,78,93,96
Seq#:15; N Pos. 108,111,114,117,120,123,129,135,138,141,144,147,156,159,165
Seq#:15; N Pos. 168,171,183,189,192,195,201,204,207,213,228,231,234,237,240
Seq#:15; N Pos. 243,249,255,264,270,276,285,288,294,297,300,309,315,318,321
Seq#:15; N Pos. 324,333,336,342,351,354,357,360,363,375,378,384,393,396,399
Seq#:15; N Pos. 402,408,432,438,441,444,447,450,456,459,468,480,483,486,489
Seq#:15; N Pos. 498,504,507,513,516,519,528,534,537,543,552,555,558,561,567
Seq#:15; N Pos. 573,579,582,585,588,591,594,597,600,624,627,633,636,645,648
Seq#:15; N Pos. 654,657,660,669,672,675,684,687,690,693,696,705,708,711,714
Seq#:15; N Pos. 723,735,738,750,762,774,777,786,789,795,807,810,816,822,825
Seq#:15; N Pos. 828,831,855,861,864,870,879,885,888,897,900,903,909,915,921
Seq#:15; N Pos. 924,927,933,939,945,948,957,960,963,966,969,975
Seq#:16; N Pos. 6,9,21,33,36,45,51,60,66,69,72,87,90,93,102,105,111,114,117
Seq#:16; N Pos. 123,135,150,153,156,162,165,171,177,192,201,210,219,222,228
Seq#:16; N Pos. 234,240,243,246,249,261,267,276,279,282,288,291,300,309,312
Seq#:16; N Pos. 318,321,324,327,333,345,348,357,363,366,369,372,375,381,387
Seq#:16; N Pos. 396,399,408,411,414,423,426,429,432,438,441,444,453,462,468
Seq#:16; N Pos. 471,477,480,483,501,507,510,513,516,519,525,528,534,543,552
Seq#:16; N Pos. 555,558,561,570,573,579,582,585,594,597,600,603,609,615,618
Seq#:16; N Pos. 621,624,627,630,633,636,639,642,645,648,651,654,663,669,675
Seq#:16; N Pos. 678,681,687,690,696,699,702,705,708,714,726,738,741,747,750
Seq#:17; N Pos. 3,6,12,15,27,36,42,51,60,66,69,72,87,90,93,96,108,114

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 10/12/2004
PATENT APPLICATION: US/10/009,445B TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
Output Set: N:\CRF4\10122004\J009445B.raw

Seq#:17; N Pos. 123,126,129,132,135,147,156,168,171,174,180,195,204,210,213
Seq#:17; N Pos. 216,219,222,228,231,240,243,252,255,258,261,270,276,279,285
Seq#:17; N Pos. 288,291,300,306,309,315,324,327,333,339,345,351,354,357,360
Seq#:17; N Pos. 363,366,369,372,396,399,402,405,408,417,420,426,429,432,441
Seq#:17; N Pos. 444,447,456,459,462,465,468,471,474,477,480,483,486,489,492
Seq#:17; N Pos. 495,501,507,516,519,522,525,534,537,543,546,552,567,573,576
Seq#:17; N Pos. 579,582

Use of <220> Feature (NEW RULES):

Error Explanation: 2

Sequence(s) are missing the <220> Feature and associated headings.

Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence" or "Unknown". Please explain source of genetic material in <220> to <223> section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp.29631-32) (Sec. 1.823 of new Rules)

3eg#:2,4,6,8,10,12,20,23

VERIFICATION SUMMARY DATE: 10/12/2004
PATENT APPLICATION: US/10/009,445B TIME: 11:51:42

Input Set : D:\14094-20009.00 - Substitute Seqlist.txt
Output Set: N:\CRF4\10122004\J009445B.raw

L:164 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:2, <213>
ORGANISM:Unknown
L:164 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:2, <213>
ORGANISM:Unknown
L:164 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2, Line#:164
L:355 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:4, <213>
ORGANISM:Unknown
L:355 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:4, <213>
ORGANISM:Unknown
L:355 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4, Line#:355
L:541 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:6, <213>
ORGANISM:Unknown
L:541 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:6, <213>
ORGANISM:Unknown
L:541 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6, Line#:541
L:699 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:8, <213>
ORGANISM:Unknown
L:699 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:8, <213>
ORGANISM:Unknown
L:699 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:8, Line#:699
L:836 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:10, <213>
ORGANISM:Unknown
L:836 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:10, <213>
ORGANISM:Unknown
L:836 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:10, Line#:836
L:992 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:12, <213>
ORGANISM:Unknown
L:992 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:12, <213>
ORGANISM:Unknown
L:992 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:12, Line#:992
L:1059 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
M:341 Repeated in SeqNo=13
L:1105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14 after pos.:0
M:341 Repeated in SeqNo=14
L:1147 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0
M:341 Repeated in SeqNo=15
L:1193 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
M:341 Repeated in SeqNo=16
L:1231 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0
M:341 Repeated in SeqNo=17
L:1263 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
M:341 Repeated in SeqNo=18
L:1405 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:20, <213>
ORGANISM:Unknown
L:1405 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:20, <213>
ORGANISM:Unknown
L:1405 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:20, Line#:1405
L:1484 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0
M:341 Repeated in SeqNo=21
L:1614 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:23, <213>
ORGANISM:Unknown
L:1614 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:23, <213>
ORGANISM:Unknown

L:1614 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:23,Line#:1614
L:1678 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24 after pos.:0
M:341 Repeated in SeqNo=24